

Annotation Example: Alpha catenin in the *Leptinotarsa decemlineata* genome

For training purposes, we have implemented special instances of our BLAST and Web Apollo tools specifically to allow for training or practice annotations. If you want to take time to familiarize yourself with the various tools before annotating on an active project, feel free to use our training resources.

The training BLAST instance is located here: i5k.nal.usda.gov/training/blast

The training Web Apollo instance created for this workshop is for *Leptinotarsa decemlineata* (lepdec), the Colorado Potato Beetle. You can access the training Web Apollo instance here: apollo.nal.usda.gov/lepdec_training

Username: demo

Password: demo

Retrieve the sequence for alpha catenin for fruit fly, and download the protein sequence (available at http://www.ncbi.nlm.nih.gov/protein/NP_524219.1).

```
>gi|17737747|ref|NP_524219.1| alpha catenin, isoform A [Drosophila melanogaster]
MLKPKDKMGTLDQFQIALKWDPKNLEIRMTMSVEKTLPEPLVLQVTTLVNTKGPSKKKGKSKRASALVAAV
EKATENFIQKGEQIAYENPDITQEMLTAVDEVKKTGDAMSIAAREFSEDPCSSLKRGNMVRARNLLSAV
TRLLILADMVDVHLLLKSLLHIVEDDLNKLKNASSQDELMDNMRQFGRNAGELIKQAAKROQELKDPQLRD
DLAAARAMLKKHSTMLLTASKVYVRHPPELDDLAKVNRDFILKQVCDAVTNTISDVAOGKSSOPTDIYSGAGE
LAAALDDFDEGIVMDPMTYSEKRSRQLLEERLESITISAALMADACDTRDERERIVAECNAVRQALQDL
LSEYMSMSQKDMSNPGSLRAIDQMCRKTRDLRRQLRKAVVHDVHSDFLETTPLLDLIEAAKSGNEKKVR
EKSEIFTKHAEKLVEVANLVCMSNNEDGVKMVRYAAAQTESLCPVINAASILTVPNPKVAQENMTTY
RQAWEVQVRILTEAVDDITTIDDFLAVSENHILEDVNKCVMALQVGDARDLRLATAGAIQGRSSRVCNVVE
AEMDNYEPCIYTKRVLLEAVKVLRDQVMMKFQQRVGAAGVALSNSNSNKKDVEDNFIDASRLVYDGVREIRR
AVLMNRSSEDLDTDEFPVEDLTLTETRSRSSAHTGDQTVDEYPDISHGICTAREAMRKMTEDKQKIAQQ
VELFRREKLTFDSEVAKWDDTGNDIIFLAHKHCMIMMEMTDFTTRGRGPPLKTTMDVINAAKKISEAGTKLD
KLTREIAEQCPESSTKKDLLAYLQRIALYCHQIQITSKVKADVNQNISGELIVSGLDSATSLIQAQKNLMN
AVVLTVKSYVASTKYTRQGTVSSPIVVMKCAPEKKPLVRPEKEEVRAKVRKGSQKKVQNPIALSEF
QSPADAV
```

Use the training BLAST tool (i5k.nal.usda.gov/training/blast) to map this gene back to the *Leptinotarsa decemlineata* (Colorado Potato Beetle) genome.

- In the BLAST page, check the *Leptinotarsa decemlineata* box on the left.
- In the right panel, check both the “Genome Assembly” and “Transcript” boxes.
- Paste the fruit fly sequence from NCBI into the Query Sequence box and click Submit.

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BLAST Databases

Organisms Leptinotarsa decemlineata

All organisms
 Leptinotarsa decemlineata

Nucleotide
 Genome Assembly - Ldec.genome.10062013_new_ids.fa
 Transcript - LDEC_new_ids.fna

Peptide
 Protein - LDEC_new_ids.faa

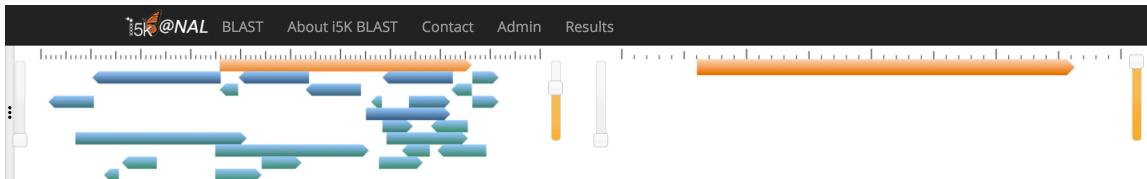
Query Sequence
Your sequence is detected as peptide:
NLMN
AVLTVKYVASTKYTRQGTVSSPIVWWKMK
APEKKPLVLRPEKPEEVRAKVRKGSGKKVQNP
HALSEF
QSPADAV

Or load it from disk
 No file selected.

Program

Blast shows a hit to one gene model (LDEC001070-RA) and eight HSPs on Scaffold1. By inspecting the HSPs in the Subject and Query panels along the top, you can verify that the HSPs are consistent in order and organization. Click on the  lepedec button to open the HSPs for Scaffold1 in the genome browser.

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Showing 1 to 9 of 25 entries

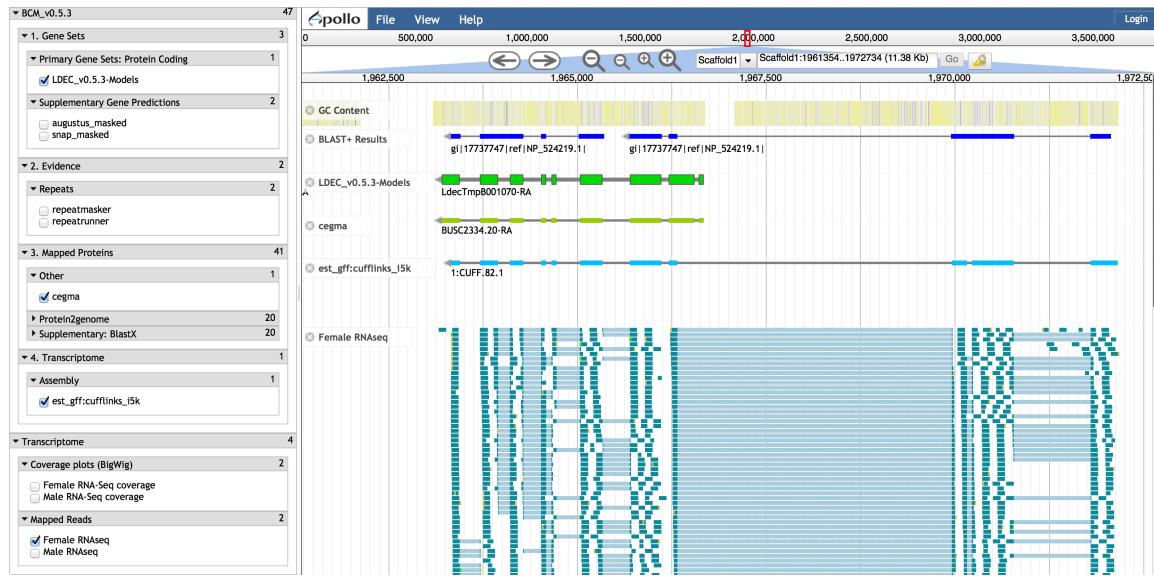
blastdb	qseqid	sseqid	pident	length	mismatch
lepedec	gi 17737747 ref NP_524219.1	LDEC001070-RA	82.45	507	86
 lepedec	gi 17737747 ref NP_524219.1	Scaffold1	73.93	280	51
 lepedec	gi 17737747 ref NP_524219.1	Scaffold1	78.17	142	31
 lepedec	gi 17737747 ref NP_524219.1	Scaffold1	78.95	38	8
 lepedec	gi 17737747 ref NP_524219.1	Scaffold1	66.84	193	13
 lepedec	gi 17737747 ref NP_524219.1	Scaffold1	76.79	112	26
 lepedec	gi 17737747 ref NP_524219.1	Scaffold1	89.13	92	10
 lepedec	gi 17737747 ref NP_524219.1	Scaffold1	85.71	42	6

36 *pgnl|Leptinotarsa_decemlineata_transcript_v0.5.1|LDEC001070-RA*
37 Length=1941
38 Score = 842 bits (2176), Expect = 0.0, Method: Compositional matrix adjust.
39 Identities = 418/507 (82%), Positives = 446/507 (88%), Gaps = 3/507 (1%)
40 Frame = +1
41 Sbjct 301 MNGOKSESLNRAIDNGMRKTRDLRQLRKAVDHVSISLET PLL L1+A+H+NKEK 488
42 Query 358 MSQKDNPSGLSRAIDQMCRKTRDLRQLRKAVDHVSISLET PLL L1+A+H+NKEK 417
43 Sbjct 301 M NGOKSESLNRAIDNGMRKTRDLRQLRKAVDHVSISLET NVPLLV1KAQNGNEK 488
44 Query 418 KVKRESEITFHAKELVVEANLVCMSMSNEDGVKMYRVAQQAEQESI,CPQVINAASILTVR 477
45 +V E + +FTHH+ KLVVEANLVCMSMSNEDGVKMYRVAQQAEQIE+LCP+VINA IL R
46 Sbjct 481 EVEEYAVFTEHFSNKLVVEANLVCMSMSNEDGVKMYRVAQQAEQEN,CPFEVINARILAR 668
47 Frame = +1
48 Sbjct 481 PNSKVQAENMTTIVRQAWEEQVRLTEAVIDDTTTDIDLAVASENHILEDVNKVCMALQGD 537
49 Sbjct 661 P SKVQAENM++WEE VRILTEAVIDDTTTDIDLAVASENHILEDVNKVCLAIQGD 848
50 Sbjct 661 PRSKVQAENKAQFQSWEHNRVRLTEAVIDDTTTDIDLAVASENHILEDVNKVCLAIQGD 848
51 Query 478 ARDLRATAGAQGSRVRCNVEAADMNEYPCYTKRVLCAWKVLRDVYMKTFDVRGAA 597
52 Sbjct 661 A L TA T+GRS+RVCNVV AEMDNEYPCYTKRVLCAWKV DQYM KF QRV A 597
53 Sbjct 661 ADLRTASIGRSRNRCNVCNVSAAEMDNEYPCYTKRVLCAWKVNDVMPKFTQRVVA 1020
54 Sbjct 841 VQALSNNSNKOVDENIDFDAISLRYDODREIRRRAVLMR+ ELD, D E + EV TLE 656
55 Sbjct 1021 VQALSNNSNKOVDENIDFDAISLRYDODREIRRRAVLMR+ ELD, D E + EV TLE 656
56 Sbjct 1021 VQALSNNSNKOVDENIDFDAISLRYDODREIRRRAVLMR+ ELD, D E + EV TLE 656
57 Sbjct 1021 VQALSNNSNKOVDENIDFDAISLRYDODREIRRRAVLMR+ ELD, D E + EV TLE 656
58 Sbjct 1021 VQALSNNSNKOVDENIDFDAISLRYDODREIRRRAVLMR+ ELD, D E + EV TLE 656
59 Query 598 VQALSNNSNKOVDENIDFDAISLRYDODREIRRRAVLMR+ ELD, D E + EV TLE 656
60 V AL NN K+VDENOFDAISLRYDODREIRRRAVLMR+ ELD, D E + EV TLE 656
61 Sbjct 1021 VQALSNNSNKOVDENIDFDAISLRYDODREIRRRAVLMR+ ELD, D E + EV TLE 656
62 Sbjct 1021 VQALSNNSNKOVDENIDFDAISLRYDODREIRRRAVLMR+ ELD, D E + EV TLE 656
63 Query 657 TRSRSAHTGQTDVEYDPSIGCTAREAMRKTEDKQKIAQQVELFRREKLTFDSEVA 716
64 VQALSNNSNKOVDENIDFDAISLRYDODREIRRRAVLMR+ ELD, D E + EV TLE 656

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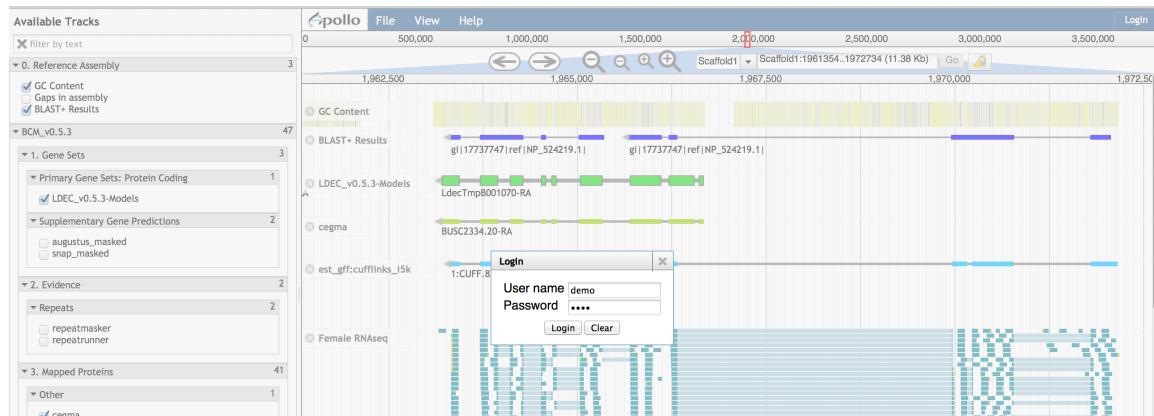
The BLAST+ Results track should be visible in the initial view of the genome browser. The initial view only shows some of the hits; Zoom out until all eight HSPs are visible.

Turn on the LDEC_v0.5.3-Models, cegma, est_gff:cufflinks and Female RNaseq tracks. Also take some time to examine the “protein2genome_Arthropoda” track to see how proteins from other arthropod species aligned to this region.

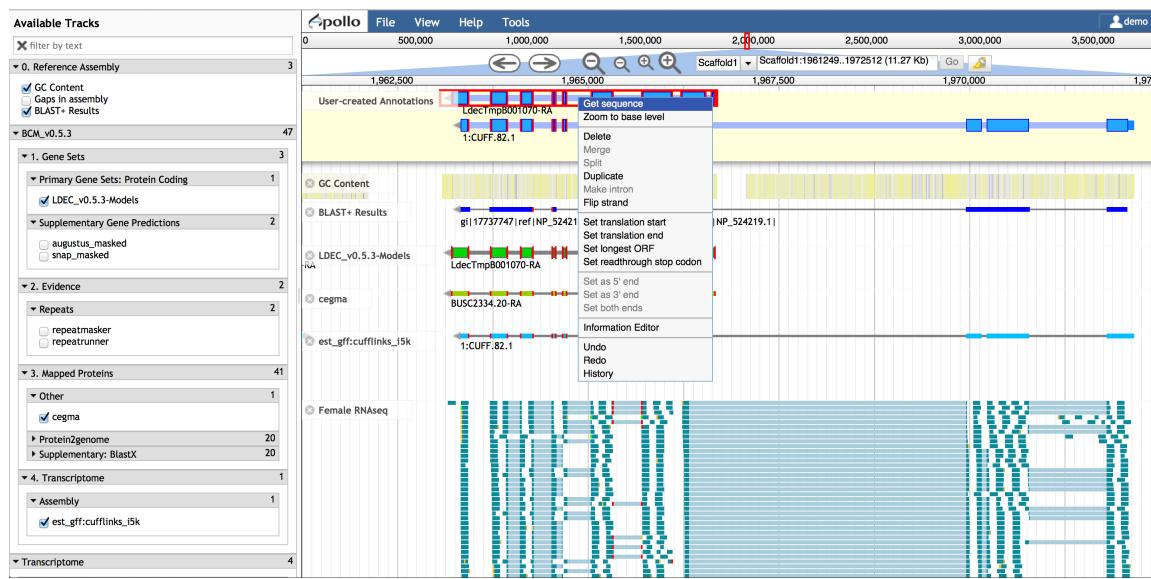


Look at the LDEC_v0.5.3 model alongside the other tracks. Clicking on an intron will highlight the entire gene model. Exons with boundaries identical to the selected model will have red edges. The LDEC_v0.5.3 model agrees with the cegma protein alignment. The cufflinks and RNAseq data support a different CDS structure for the first three exons. The BLAST results also indicate that the five-prime end of the gene may be further upstream than predicted by the LDEC_v0.5.3 model.

Log in to enable edit mode.



Click and drag both the LDEC model and the Cufflinks model into the yellow “User-created Annotations” pane at the top of the browser. Next, right-click an intron to select the entire model and click “Get sequence”. Save the translated sequence in a text file and repeat for the other gene model. To make the multiple alignment easier to follow, prepend each sequence name with a short descriptive tag.



Open a multiple sequence aligner like Clustal Omega

<http://www.ebi.ac.uk/Tools/msa/clustalo/>

Perform a multiple sequence alignment with the sequences saved from NCBI (fruit fly) and the gene models saved from Web Apollo (LDEC_v0.5.3 and Cufflinks).

Paste the three sequences into the input box and click submit.

The results show that there are differences in the five prime and three prime ends of the gene. This is more pronounced in the LDEC_v0.5.3 model (See attached Clustal report LDEC_clustal_1).

To try to get a better alignment, remove the LDEC model and rerun Clustal (see LDEC_clustal_2). The new alignment has a shorter area of disagreement at the five prime end.

In Web Apollo, zoom in on the start of the longer model. You can see that the model runs into a gap in the assembly, limiting our ability to annotate further. Zoom back out to view the entire gene and then zoom in to the three prime end of the gene. The cufflinks model does not end with a stop codon. You should

extend the exon until it includes a stop codon. You can do this by dragging the end of the exon until it includes a stop codon OR by merging the last exon from the LDEC model with the active annotation. To merge them, click on the last exon in the LDEC model and drag it up to the Cufflinks model until the box around the active annotation turns green then release the mouse button. The end of the two models should now be the same, which you can see through the red edge highlighting.

Get the new peptide sequence and use NCBI's BLASTP to search it back against the non-redundant (nr) database. The top two hits are to alpha catenin genes in *Tribolium castaneum*, the red flour beetle, and *Bombus impatiens*, a bumblebee. Use these two protein sequences along with the sequence from the annotation in another multiple-alignment (see LDEC_clustal_3). These models have better agreement at the five prime end of the gene, but there is still some disagreement with the annotation at the three prime end. Unfortunately, there is also a gap in the assembly at the three prime end, so further refinement of this model is not possible at this time. The annotation does have in-frame start and stop codons. This is the best that I can annotate this model.

Now that our new candidate gene model is annotated, delete the shorter model, leaving the Cufflinks-based model. Now we need to add information to describe this model and the actions we took to make it. Right click on the model and select "Information Editor".

- For the Name fields, enter "catenin alpha".
- On the mRNA side, click Add to add a comment, then use the drop down option to select "Annotation type: Modify an existing gene model ". Add more information to clearly state what the model is: "Annotation type: Modify an existing gene model: LdecTmpB001070-RA"
- You also need to add additional comments here as applicable to your work. In this case I also added "Result of: Adding an exon to the gene model".
- Finally click the "Approved" option in the Status section. This lets others know that you feel the annotation is complete. Even if you do not change the status the annotation will remain so you can save the URL and return to complete it later.

The screenshot shows the Apollo genome annotation tool interface. On the left, the "Available Tracks" sidebar lists various genomic resources and databases. The main area is the "Information Editor" for a gene named "catenin alpha".

Information Editor (Left Panel):

- Gene:** catenin alpha
- Status:** Approved
- DBXRefs:** DB Accession
- Pubmed IDs:**
- Gene Ontology IDs:**
- Comments:** Annotation type: Modify an existing gene model : LdecTmpB0011070-RA
Result of: Adding an exon to the gene model

Information Editor (Right Panel):

- mRNA:** catenin alpha
- Status:** Approved
- DBXRefs:** DB Accession
- Pubmed IDs:**
- Gene Ontology IDs:**
- Comments:**

Genomic View (Bottom Right):

Once this is done, simply click the X to close the Information Editor. Your modifications are already saved back to the server.

Web Apollo Workshop Example Supplemental Materials

Web Resources used:

BLAST: <https://i5k.nal.usda.gov/training/blast>

JBrowse : https://apollo.nal.usda.gov/lepdec_training/jbrowse

Web Apollo: https://apollo.nal.usda.gov/lepdec_training/

Clustal Omega: <http://www.ebi.ac.uk/Tools/msa/clustalo/>

Additional Resources

Annotation guide

LDEC_clustal_1

CLUSTAL O(1.2.1) multiple sequence alignment

```
LDEC_009905F2F303802AED9B6891B7FFF088  
gi|17737747|ref|NP_524219.1|  
Cufflinks_92BA0B7F01612DBCD26CE6DAEA73897C-----  
MLKPDKGMTLTDFAQIALKWDPKNLEIRTSVEKTLERPLVLQVTTLVNTKGPSKKKGKS  
-----MTDRFGLKWDPKNLEIRTSVEKTLERPLVLQVTTLVNTKGPSKKKGKS  
  
LDEC_009905F2F303802AED9B6891B7FFF088  
gi|17737747|ref|NP_524219.1|  
Cufflinks_92BA0B7F01612DBCD26CE6DAEA73897C-----  
KRASALVAAVEKEKATENFIQGEQIAYENPDIQEMLTADEVKKTGDMASIAAREFSEDP  
KRANALVSTVEKATENFIKEQEIQIAYENPDIDEMLAAVEEVKKTGAMSVAAREFSEDP  
  
LDEC_009905F2F303802AED9B6891B7FFF088  
gi|17737747|ref|NP_524219.1|  
Cufflinks_92BA0B7F01612DBCD26CE6DAEA73897C-----  
CSSLRKGNMVRARNLLSAVTRLLILADMDVHLLLKSLHIVEDDLNLKLNASSQELMD  
CSSLRKGNMVRARNLLSAVTRLLILADMDVHLLLKSLHVVEDDLEKLKNASSHGELD  
  
LDEC_009905F2F303802AED9B6891B7FFF088  
gi|17737747|ref|NP_524219.1|  
Cufflinks_92BA0B7F01612DBCD26CE6DAEA73897C-----  
MLSSLKSVLLCI-----QQL-  
NMRQFGRNAGELIKQAAKRQQELKDPLRDLAAARMLKHSTMLLTASKVYVRHPELD  
NIKAFGQNANEMLMQAAKRQQELKDPLRDLAAARAVLKHKSTMLLTASKVYVRHPELD  
*: . : *: ** : *:  
-----EVLRGVT--RPLSIYSLK--ITA--SNQDMHSTMSQLTK  
LAKVNRPDIILKQVCDAVNTISDVAQKGSQOPT-DIYSGAGELAAALDDPDEGIIVMPMTY  
AAKANRDYVLKVQCEAVHTINDVAQGRTQPACGPYDGPGEALAALDDPDDHVMVMEPLAY  
*: * : * : * : * : * : * : * : * : * : * : *:  
-----NQSYYIFCISFFNDVALK-WAAISEIPIECSLFLFLSVKICFKPHLOOF  
SEKRSRQLLEERLESIIASAAMADADCTRDERRERIVAEBCNA----VRQALQDLLSE-  
NEVHTRPSLEERLESIIISGAALMADSSTCRDERRERIVAEBCNA----VRQALQDLLSE-  
*: * : * : * : * : * : * : * : * : * : * : *:  
FICLOMGNKDKSESLNRRAIDNMGRKTRDLRRQRLRKAVVHDVSDSFLETNVPLLVLIKAQO  
-YMSMSQDKNSPGLSRAIDQMCRKTRDLRRQRLRKAVVHDVSDSFLETTPPLLDLIEAAK  
-YMTNMGNKDKSESLNRRAIDNMGRKTRDLRRQRLRKAVVHDVSDSFLETNVPLLVLIKAQO  
*: * : * : * : * : * : * : * : * : * : * : * : * : * : *:  
NGNEKEVEEYAVVTEHSNLKVEANLVCMSNNEDGVKMVRYAAAQIEENLCPEVINAAAR  
SGNEKKVREKSEIFTKHAKELKVEANLVCMSNNEDGVKMVRYAAAQIESLCPVINAAAS  
NGNEKEVEEYAVVTEHSNLKVEANLVCMSNNEDGVKMVRYAAAQIEENLCPEVINAAAR  
.*****: * : * : * : * : * : * : * : * : * : * : * : * : *:  
ILAARPRSKVAQENMAAFKQSWEHNVRILTEAVDDITTIDFLAVSENHILEDVNKCVLA  
ILTWRPNSKVAQENMMTYRQAEWVQRILTEAVDDITIDFLAVSENHILEDVNKCVMA  
ILAARPRSKVAQENMAAFKQSWEHNVRILTEAVDDITTIDFLAVSENHILEDVNKCVLA  
*: * : * : * : * : * : * : * : * : * : * : * : * : * : *:  
LQEGRDADTLDRTAGSIRGRSRNSRVCNVVSAEMDNYEPICIYTKRVLLEAVKVLNDQVMPKFTQ  
LQVGDDRLRATAGAIQGRSSRVCNVVVAEMDNYEPICIYTKRVLLEAVKVLNDQVMPKFTQ  
LQEGRDADTLDRTAGSIRGRSRNSRVCNVVSAEMDNYEPICIYTKRVLLEAVKVLNDQVMPKFTQ  
*: * : * : * : * : * : * : * : * : * : * : * : * : * : *:  
RVQVAVQALGNNNPPKEVDENDFIDASRLVYDGVREREAVLMNRADEDLLP-EVELDEN  
RVGAAGVLSNNSNKKDVEDNDFIDASRLVYDGVREREAVLMNRSSEDLDTTEFEPVED  
RVQVAVQALGNNNPPKEVDENDFIDASRLVYDGVREREAVLMNRADEDLLP-EVELDEN  
*: * : * : * : * : * : * : * : * : * : * : * : * : * : *:  
YTLETRSKSAAHTGEHVDEYPDISINGTAREAMGKMPPEDKQKILQOQVEFFRSEKLKFD  
LTLETRSKSAAHTGDQTVDYEYPDISINGTAREAMRKTMBEDQKIAQQVLEFRREKLTFD  
YTLETRSKSAAHTGEHVDEYPDISINGTAREAMGKMPPEDKQKILQOQVEFFRSEKLKFD  
*****: * : * : * : * : * : * : * : * : * : * : * : * : *:  
REVAKWDDTGNDIIVLAKHCMCIMMEMTDFTTRGRGPLKTTMDVINAACKISEAGTKLDKL  
SEVAWKWDDTGNDIIVLAKHCMCIMMEMTDFTTRGRGPLKTTMDVINAACKISEAGTKLDKL  
REVAKWDDTGNDIIVLAKHCMCIMMEMTDFTTRGRGPLKTTMDVINAACKISEAGTKLDKL  
*****: * : * : * : * : * : * : * : * : * : * : * : * : *:  
TRQIAEQCPESSTKQDLLAYLQRIALYCHQMNITSVKVADVNQISGELIVSGLDSATSLI  
TREIAEQCPESSTKQDLLAYLQRIALYCHOIQTTSVKVADVNQISGELIVSGLDSATSLI  
TRQIAEQCPESSTKQDLLAYLQRIALYCHQMNITSVKVADVNQISGELIVSGLDSATSLI  
*: * : * : * : * : * : * : * : * : * : * : * : * : *:  
QAQKNLMLNAVVLTVKSSYVASTKYPROGTIAVSDFSLKQIMFEHICQRFCMKICYEFG  
QAQKNLMLNAVVLTVKSSYVASTKYTRQGTWSPPIVWWKMKAPE-----K  
QAQKNLMLNAVVLTVKSSYVASTKYPROGTIAV-----  
*****: * : * : * : * : * : * : * : * : * : * : *:  
VPLS-KQVPTDLK-----  
KPLVRPEKPEEVRAKVRKGSQKKVQNPPIHALSEFQSPADAV  
-----
```

LDEC_clustal_2

CLUSTAL O(1.2.1) multiple sequence alignment

gi 17737747 ref NP_524219.1 Cufflinks_92BA0B7F01612DBCD26CE6DAEA73897C	MLKPDKGTLTDFQIALWKDPKNLEIRTMSVEKTLEPLVLQVTTLVNTKGPSKKKGKS -----MTDRFGLKWDPKNLEIRTMSEVKTLERPLVLQVTTLVNTKGPSKKKGKS *:****:*****:*****:*****:*****:*****:*****:*****:*****: KRASALVAAVEKATENFIQKGEQIAYENPDTIQEMLTADEVKKTG DAMSIAAREFSEDP KRANALVSTVEKATENFIQKGEQIAYENPDTDEMLAAVEEVVKKTGTAMSVAAREFSEDP ***:****:*****:*****:*****:*****:*****:*****:*****: CSSLRGNMVRARNLLSAVTRLLILADMVDVHLLLKSLHIVEDDLNLKLNKASSQDELMD CSSLRGNMVRARNLLSAVTRLLILADMVDVHLLLKSLHVVEDDLEKLNKNA SHGEELLD *****:*****:*****:*****:*****:*****:*****:*****: NMROFGRNAGELIKQAAKROELKDPLQRDLAARAMLKKHSTMLLTASKVYVRHPELD NIKAFQGNANELMQAAKROELKDPLQRDLAARAVLKHKHSTMLLTASKVYVRHPELA *:****:*****:*****:*****:*****:*****: LAKVN RD F ILKQVCDAV NT IS DVA QGKSSQ PT -DIYSGAGEL A A LDD P DEGIV M DPM TY AAKANRDY V LKVQVCEAVHTINDVAQGRTPQ PAC GPYDGP GEL A A L D D F DD H M V M E PL A Y **:***:****:*.****: * : * . * ****:*****:*****:*****: SEKRSRQLL ERLES I S A A L M A D C T R D E R R E R I V A E C N A V R Q A L Q D L L S E Y M S N M S NEV H T R P S L E R L E S I S G A A L M A D S S C T R D E R R E R I V A E C N A V R Q A L Q D L L S E Y M T N M G . * : **:*****:*****:*****:*****:*****: QKD NSPGLS R A ID Q M C R K T R D L R Q L R K A V V D H V S D S F L E T T P L L D I E A A K S G N E K K V N K D K S E S L N R A I D N M G R K T R D L R Q L R K A V V D H V S D S F L E T N P L L V L I K A A Q N G N E K E V *:***:*.****:*****:*****:*****:*****: REKSEI F T K H A E K L V E V A N L V C M S S N N E D G V K M V R Y A A A Q I E S L C P Q V I N A A S I L T V R P N EY AVV F T E H S N K L V E V A N L V C M S S N N E D G V K M V R Y A A A Q I E N L C P E V I N A A R I L A A R P R . * : ***:*****:*****:*****:*****: SKVAQEN M T T Y R Q A W E V Q V R I L T E A V D D I T I D D F L A V S E N H I L E D V N K C V M A L Q V G D A R SKVAQEN M A A F K Q S W E N H V R L I T E A V D D I T I D D F L A V S E N H I L E D V N K C V L A L Q E G D A D *****:*****:*****: DLR AT AGAI QGRSSRV CNV V E A E M D Y E P C I Y T K R V L E A V K V L R D Q V M M K F D Q R V G A A V G TLD R T A S G I R G R S N R V C N V V S A E M D Y E P C I Y T K R V L E A V K V L N D Q V M P K F T Q R V Q V A V Q * ***:***:*****:*****: ALS NSNS N K D V E N D F I D A S R L V Y D G V R E I R R A V L M N R S S E D L D T E F E P V E D L T L E T R S A L G N P P K E V D E N D F I D A S R L V Y D G V R E I R R A V L M N R A D E D L D P E - D V E L D E N Y T L E T R S *:***:*****:*****: RSS A H T G D Q T V D E Y P D I S G I C T A R E A M R K M T E D K Q K I A Q Q V E L F R R E K L T F D S E V A K W D R S S A H T G E H G V D E Y P D I S G I T T A R E A M G K M P E D K Q K I L Q V E F F R S E K L K P D R E V A K W D *****:*****: DTGNDI I F L A K H M C M I M M E T D F T R G R G P L K T T M D V I N A A K K I S E A G T K L D K L T R Q I A E Q DTGNDI I V L A K H M C M I M M E T D F T R G R G P L K T T M D V I N A A K K I S E A G T K L D K L T R Q I A E Q *****:*****: C P E S T K D D L L A Y L Q R I A L Y C H Q I Q I T S K V K A D V Q N I S G E L I V S G L D S A T S L I Q O A K N L M C P E S T K D D L L A Y L Q R I A L Y C H Q M N I T S K V K A D V Q N I S G E L I V S G L D S A T S L I Q O A K N L M *****:*****: NA V A L T V K Y S Y V A S T K Y T R Q G T V S P I V V W K M K A P E K K P L V R P E K P E E V R A K V R K G S Q K K NA V A L T V K S S Y V A S T K Y P R O G T I A V ----- *****: V Q N P I H A L S E F Q S P A D A V -----
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LDEC_clustal_3

CLUSTAL O(1.2.1) multiple sequence alignment

B_im-p-gi|350397044|ref|XP_003484750.1|
T_cas-gi|91076138|ref|XP_970159.1|
cufflinks-362CFAFB1F42C3D289AF73E188844BA8

MSDHFGPITLKWDPKNLIRMTSVEKTLEPLVLQVTTLVNTKGPSKKKGSKRASALVG
MNDHFG---LKWDPKNLIRMTSVEKTLEPLVLQVTTLVNTKGPSKKKGSKRANALVS
MTDRFG---LKWDPKNLIRMTSVEKTLEPLVLQVTTLVNTKGPSKKKGSKRANALVS
*.**.*****:*****:*****:*****:*****:*****:*****:*****:*****:

TVEKATENFIKEKGEOIAYENPDITAEMLSAVEEVKKTGAMSIAAREFSEDPCSSLKGRN
TVEKATENFIKEKGEOIAYENPDITOEMLSAVEEVVKTGAMSIAAREFSEDPCSSLKGRN
TVEKATENFIKEKGEOIAYENPDITDEMLAAVEEVKKTGAMSVAAREFSEDPCSSLKGRN
*****:*****:*****:*****:*****:*****:*****:*****:*****:

MVRAARNLLSAVTRLLILADMDVDHVLLLKSLLHVVEDDLKLNASSQGELLENIKOFGRN
MVRAARNLLSAVTRLLILADMDVDHVLLLKSLLHVVENDIEKLKNASSQGELLDNIKAFGQN
MVRAARNLLSAVTRLLILADMDVDHVLLLKSLLHVVEDDLKLNASSHGEELLDNIKAFGQN
*****:*****:*****:*****:*****:*****:*****:*****:*****:

ASELMNQAARKQQELKDPQLRDDLAAARAVLKKHSTMLLTASKVYVRHPELAAKANRDY
ANELMNQAARKQQELKDPQLRDDLAAARAVLKKHSTMLLTASKVYVRHPELAAKANRDY
ANELMNQAARKQQELKDPQLRDDLAAARAVLKKHSTMLLTASKVYVRHPELAAKANRDY
*.*****:*****:*****:*****:*****:*****:*****:*****:*****:

VLKVQCEAVINTINDVAQGRTPQPATGPYDGPGLAAALDDFDHMVMEPLAYNEVHTRPS
VLKVQCEAVINTINDVAQGRTPQPATGPYDGPGLAAALDDFDHMVMEPLAYNEVHTRPS
VLKVQCEAVINTINDVAQGRTPQPATGPYDGPGLAAALDDFDHMVMEPLAYNEVHTRPS
*****:*****:*****:*****:*****:*****:*****:*****:*****:

LEERLESIISSGAALMADSSCTRDERERRERIVAECNAVRQALQDLLSEYMMNNMGVKEQSGL
LEERLESIISSGAALMADSSCTRDERERRERIVAECNAVRQALQDLLSEYMSNIGNKEKSES
LEERLESIISSGAALMADSSCTRDERERRERIVAECNAVRQALQDLLSEYMTNMGNKDSES
*****:*****:*****:*****:*****:*****:*****:*****:*****:

ERAIDHMCRKTRDLRQLRKAADVHDVSDFSLTSPVLLVIEAARNGRDKEVEEYALVFT
NRAIDNMGKTRDLRQLRQLRKAADVHDVSDFSLTNPVLLVLIKAAQNGNEKEVEEPAVFT
NRAIDNMGKTRDLRQLRKAADVHDVSDFSLTNPVLLVLIKAAQNGNEKEVEEYAVVFT
*:***.*:*****:*****:*****:*****:*****:*****:*****:*****:

EHANKLVEVANLVCMSGNSEDGVKMVRYAAQIGNLCPVQVINAARVLAARNRSKVALDNM
EHSNKLVEVANLVCMSNSNEDGVKMVRYAAQIDNLCPVQVINAARILAARPRSKVAQENN
EHSNKLVEVANLVCMSNSNEDGVKMVRYAAQIENLCPVQVINAARILAARPRSKVAQENN
*:*****:*****:*****:*****:*****:*****:*****:*****:

EVFRQAWENQVRVLTEAVDDITIIDDFLAVSENHILEDVNKCVLALQEGDADTLDRTAG
DAFKQSWEVNRVILTEAVDDITIIDDFLAVSENHILEDVNKCVLALQEGDADTLDRTAG
AAFKQSWEVNRVILTEAVDDITIIDDFLAVSENHILEDVNKCVLALQEGDADTLDRTAG
*:*****:*****:*****:*****:*****:*****:*****:*****:

IRGRSARVCNVVQAEMDNYPICITYTKRVLIAEVKVLREQVMPKFAQRVVEAVDALGSNP
IRGRSNRVCNVVTAEMDNYPICITYTKRVLIAEVKVLNDQVMPKFSQRVQAVQALSSVPT
IRGRSNRVCNVVQAEMDNYPICITYTKRVLIAEVKVLNDQVMPKFTQRVQAVQALGNNP
*****:*****:*****:*****:*****:*****:*****:*****:

DVEDNDFIDASRLVYDGVREIRRAVLMNRADEDLDPEDVELDEHYTELRSKSSAQTGEH
EVDENDFIDASRLVYDGVREIRRAVLMNRADEDLDPEDVELDENYTLELRSKSSAHTGEH
EVDENDFIDASRLVYDGVREIRRAVLMNRADEDLDPEDVELDENYTLELRSKSSAHTGEH
*:*****:*****:*****:*****:*****:*****:*****:

GVDEYPEISGITTAREAMRKMPPEEKQILQOQEYFKSEKLKFDEKAVWDDAGNDIIVL
GVDEYPEISGITTAREAMGKMPPEEKQILQOQEYFKSEKLKFDEKAVWDDTGNDIIVL
GVDEYPEISGITTAREAMGKMPPEEKQILQOQEFFFSEKLKFDEKAVWDDTGNDIIVL
*****:*****:*****:*****:*****:*****:*****:

AKHMCMIMMEMTDFTTRGRGPLKTTMDVINAAKKISEAGTKLDKLTRQIAODCPESSTKKD
AKHMCMIMMEMTDFTTRGRGPLKTTMDVINAAKKISEAGTKLDKLTRQIAECPESSTKKD
AKHMCMIMMEMTDFTTRGRGPLKTTMDVINAAKKISEAGTKLDKLTRQIAECPESSTKKD
*****:*****:*****:*****:*****:*****:

LLAYLQRIALYCHQMNITSKVKADVNQINSIGELIVSGLDSATSLIQAQKNLMLNAVVLTVKA
LLAYLQRIALYCHQMNITSKVKADVNQINSIGELIVSGLDSATSLIQAQKNLMLNAVVLTVKA
LLAYLQRIALYCHQMNITSKVKADVNQINSIGELIVSGLDSATSLIQAQKNLMLNAVVLTVKA
*****:*****:*****:*****:*****:

SYVASTKYPRQGTISPIVVWKMKP-----EKKPLVPERPEEVRAKV
SYVASTKYPRQGTIAVSDFSILKQIMFEHICRFECMKICYEFGVPLS-KQVPTDLK--
*****:*****:*****:*****:*****:

RKGSQKKVQNPPIHALSEFQSPTESV
RKGSQKKVQNPPIHALSEFQSPTESI
